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TECH CENTER 1600/2900

SEQUENCE LISTING

<110> McKeon, F.
Kayako, K.
Ryeom, S.

<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN
USES AND REAGENTS RELATED THERETO

<130> HMV-048.01

<140> 09/575,580

<141> 2000-05-22

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<170> PatentIn Ver. 2.1

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 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60
 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110
 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125
 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
 130 135 140
 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
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 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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 35 40 45
 Leu Thr Asp Phe Ser Asp Leu Pro Asn Ser Leu Phe Ala Cys Asn Val
 50 55 60

His Gln Ser Val Phe Glu Glu Glu Glu Ser Lys Glu Lys Phe Glu Gly
 65 70 75 80
 Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe Lys Ser
 85 90 95
 Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala Ala Arg
 100 105 110
 Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Pro
 115 120 125
 Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu
 130 135 140
 His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro
 145 150 155 160
 Ser Ser Pro Ser Val Gly Trp Lys Pro Ile Ser Asp Ala Thr Pro Val
 165 170 175
 Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu
 180 185 190
 Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val
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 His Val Cys Asp Ser Asp Met Glu Arg Glu Glu Asp Pro Lys Thr Ser
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 Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly Leu Pro Pro Phe
 225 230 235 240
 Gly His

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 <213> Homo sapiens

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 35 40 45
 Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
 50 55 60
 Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
 65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
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<211> 170

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<213> Homo sapiens

<400> 7

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35 40 45

Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His
50 55 60

Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu
65 70 75 80

Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp
85 90 95

Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu
100 105 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro
115 120 125

Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu

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135

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Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr
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<210> 8

<211> 197

<212> PRT

<213> Cricetulus griseus

<400> 8

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20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg Met
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Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
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Pro Ile His Leu Ser
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<210> 9

<211> 207

<212> PRT

<213> *Caenorhabditis elegans*

<400> 9

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Ile	Val	Thr	Gln	Val	Pro	Glu	Asp	Val	Phe	Asp	Asn	Lys	Gln	Asp	Lys	
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Ala	Asn	Phe	Ser	Ser	Leu	Phe	Thr	Gln	Ile	Glu	Lys	Asp	Ile	His	Phe	
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Glu	Asn	Ala	Thr	Ala	Ala	Lys	Leu	Ile	Val	Gln	Gly	Phe	Ser	Phe	Lys	
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Gly	His	Glu	Leu	Lys	Ala	Phe	Phe	Ala	Gln	Arg	Ile	Tyr	Met	Ser	Ala	
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Pro	Pro	Val	Val	Cys	Asn	Phe	Asp	Leu	Met	Ala	Arg	Leu	Ala	Ser	Phe	
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Ala	Ile	Asp	Glu	Lys	Tyr	Glu	Val	His	Asn	Gly	Asp	Glu	Leu	Thr	Pro	
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Ala	Ile	Ile	Val	His	Pro	Cys	Glu	Thr	Pro	Ile	Asp	Val	Pro	Ser	Ala	
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<213> *Saccharomyces cerevisiae*

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35

40

45

Leu Ile Ile Leu Lys Arg Phe Lys Arg Ile Leu Leu Ile Cys Pro Ser
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 100 105 110
 Ser Pro Pro Ala Ser Pro Pro Pro Glu Phe Asp Phe Ser Lys Cys Glu
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 Asp Ala Pro Gln Arg His Ile Gln Ser His Ile Gln Gln Asp Gln Gln
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 145 150 155 160
 Asn Asn Gly Thr Phe Thr Leu Leu Lys Ser Lys Val Gly Ala Ile Thr
 165 170 175
 Ile Asp Arg Cys Pro Thr Asn Asp Gly Asn Gly Gln Met Gln Leu Ala
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 Asp Asp Asp
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<210> 11

<211> 163

<212> PRT

<213> Schizosaccharomyces pombe

<400> 11

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 35 40 45
 Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val
 50 55 60
 His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser
 65 70 75 80

Val Asp Gln Ser Leu Gln Val Pro Lys Phe Glu Lys Asn Trp Leu Ile
85 90 95

Ser Pro Pro Gly Ser Pro Pro Val Gly Trp Glu Pro Ile Val Glu Glu
100 105 110

Ser Pro Asn Ser Gln His Leu Ala His Asp Ile Gln Leu Lys Leu Asp
115 120 125

Glu Leu Gly Asn Ala Leu Leu Asn Asp His Ser Ala Gly Pro Gln Ile
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Phe Glu His

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<213> Homo sapiens

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<212> DNA

<213> Mus musculus

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<212> DNA

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<212> PRT

<213> Mus musculus

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35	40	45	
Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Val Gln Glu Gln			
50	55	60	
Lys Glu Arg Phe Glu Ala Leu Phe Thr Leu Tyr Asp Asp Gln Val Thr			
65	70	75	80
Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys			
85	90	95	
Pro Ala Arg Ala Arg Ile Glu Leu His Glu Ser Glu Phe His Gly Arg			
100	105	110	
Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Val Ser Gly Glu Ala Arg			
115	120	125	
Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Thr Lys Gln Phe Leu Ile			
130	135	140	
Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser Glu Asp Ala			
145	150	155	160
Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser Lys Leu Gly			
165	170	175	
Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser			
180	185	190	
Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu Glu Asp Thr			
195	200	205	
Lys Asn Pro Lys Gln Lys Ile Thr Gln Thr Arg Arg Pro Glu Ala Pro			
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<212> DNA

<213> Mus musculus

<400> 25

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<212> DNA

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<213> Mus musculus

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<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: general structure

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<221> SITE

<222> (6)

<223> Xaa=any amino acid residue

<400> 28

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<210> 29

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<223> Description of Artificial Sequence: calcineurin

antagonist

<400> 29

Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu
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<210> 30

<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: calcineurin
antagonist

<400> 30

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<210> 31

<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: EGF-derived
peptide

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Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
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<210> 32

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-derived
peptide

<400> 32

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
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<210> 33

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pH-dependent
membrane-binding internalizing peptide

<220>
 <221> SITE
 <222> (1)
 <223> Xaa=preferably a unique residue, such as Cys or Lys, that facilitates chemical conjugation of the internalizing peptide to a targeting protein conjugate

<220>
 <221> SITE
 <222> (2)..(3)
 <223> Xaa=residues selected to modulate the affinity of the internalizing peptide for different membranes

<400> 33
 Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
 1 5 10 15
 Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
 20 25 30

<210> 34
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide substrate

<400> 34
 Gly Asn Ala Ala Ala Ala Arg Arg
 1 5

<210> 35
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (4)..(75)

<220>
 <223> Description of Artificial Sequence: synthetic construct

<400> 35
 cat atg ggt ggc tgc cgt ggc gat atg ttc ggt tgc ggt gct cct cca 48
 Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro
 1 5 10 15

aaa aag aag aga aag gta gct gga ttc
 Lys Lys Lys Arg Lys Val Ala Gly Phe
 20

75

<210> 36
 <211> 24
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 36
 Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
 1 5 10 15
 Lys Lys Arg Lys Val Ala Gly Phe
 20

<210> 37
 <211> 225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4)..(225)

<400> 37
 cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly
 1 5 10 15
 agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96
 Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
 20 25 30
 ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144
 Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr
 35 40 45
 ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln
 50 55 60
 act cat caa gtt tct cta agt aag caa gga ttc 225
 Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe
 65 70

<210> 38
 <211> 74
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 38
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
 35 40 45
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 50 55 60
 His Gln Val Ser Leu Ser Lys Gln Gly Phe
 65 70

<210> 39
 <211> 912
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4)..(912)

<400> 39
 cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cgg gag gtt ccg 48
 Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro 15
 1 5 10 15
 cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg gcg 96
 Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala 30
 20 25 30
 agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca 144
 Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr 45
 35 40 45
 cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg 192
 Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser 60
 50 55 60
 gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg 240
 Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro

65					70					75						
gag	gtc	ccc	cgg	acg	cgg	cgt	ccc	gtt	tcc	ggg	gcg	gtt	ttg	tcc	ggc	288
Glu	Val	Pro	Arg	Thr	Arg	Arg	Pro	Val	Ser	Gly	Ala	Val	Leu	Ser	Gly	
80					85					90					95	
ccg	ggg	cct	gcg	cgg	gcg	cct	ccg	cca	ccc	gct	ggg	tcc	gga	ggg	gcc	336
Pro	Gly	Pro	Ala	Arg	Ala	Pro	Pro	Pro	Pro	Ala	Gly	Ser	Gly	Gly	Ala	
				100					105					110		
gga	cgc	aca	ccc	acc	acc	gcc	ccc	cgg	gcc	ccc	cga	acc	cag	cgg	gtg	384
Gly	Arg	Thr	Pro	Thr	Thr	Ala	Pro	Arg	Ala	Pro	Arg	Thr	Gln	Arg	Val	
			115					120					125			
gcg	act	aag	gcc	ccc	gcg	gcc	ccg	gcg	gcg	gag	acc	acc	cgc	ggc	agg	432
Ala	Thr	Lys	Ala	Pro	Ala	Ala	Pro	Ala	Ala	Glu	Thr	Thr	Arg	Gly	Arg	
		130					135					140				
aaa	tcg	gcc	cag	cca	gaa	tcc	gcc	gca	ctc	cca	gac	gcc	ccc	gcg	tcg	480
Lys	Ser	Ala	Gln	Pro	Glu	Ser	Ala	Ala	Leu	Pro	Asp	Ala	Pro	Ala	Ser	
	145					150					155					
acg	gcg	cca	acc	cga	tcc	aag	aca	ccc	gcg	cag	ggg	ctg	gcc	aga	aag	528
Thr	Ala	Pro	Thr	Arg	Ser	Lys	Thr	Pro	Ala	Gln	Gly	Leu	Ala	Arg	Lys	
160					165					170					175	
ctg	cac	ttt	agc	acc	gcc	ccc	cca	aac	ccc	gac	gcg	cca	tgg	acc	ccc	576
Leu	His	Phe	Ser	Thr	Ala	Pro	Pro	Asn	Pro	Asp	Ala	Pro	Trp	Thr	Pro	
				180					185					190		
cgg	gtg	gcc	ggc	ttt	aac	aag	cgc	gtc	ttc	tgc	gcc	gcg	gtc	ggg	cgc	624
Arg	Val	Ala	Gly	Phe	Asn	Lys	Arg	Val	Phe	Cys	Ala	Ala	Val	Gly	Arg	
			195					200					205			
ctg	gcg	gcc	atg	cat	gcc	cgg	atg	gcg	gcg	gtc	cag	ctc	tgg	gac	atg	672
Leu	Ala	Ala	Met	His	Ala	Arg	Met	Ala	Ala	Val	Gln	Leu	Trp	Asp	Met	
		210					215					220				
tcg	cgt	ccg	cgc	aca	gac	gaa	gac	ctc	aac	gaa	ctc	ctt	ggc	atc	acc	720
Ser	Arg	Pro	Arg	Thr	Asp	Glu	Asp	Leu	Asn	Glu	Leu	Leu	Gly	Ile	Thr	
	225					230					235					
acc	atc	cgc	gtg	acg	gtc	tgc	gag	ggc	aaa	aac	ctg	ctt	cag	cgc	gcc	768
Thr	Ile	Arg	Val	Thr	Val	Cys	Glu	Gly	Lys	Asn	Leu	Leu	Gln	Arg	Ala	
240					245					250					255	
aac	gag	ttg	gtg	aat	cca	gac	gtg	gtg	cag	gac	gtc	gac	gcg	gcc	acg	816
Asn	Glu	Leu	Val	Asn	Pro	Asp	Val	Val	Gln	Asp	Val	Asp	Ala	Ala	Thr	
				260					265					270		
gcg	act	cga	ggg	cgt	tct	gcg	gcg	tcg	cgc	ccc	acc	gag	cga	cct	cga	864
Ala	Thr	Arg	Gly	Arg	Ser	Ala	Ala	Ser	Arg	Pro	Thr	Glu	Arg	Pro	Arg	
			275					280					285			
gcc	cca	gcc	cgc	tcc	gct	tct	cgc	ccc	aga	cgg	ccc	gtc	gag	gaa	ttc	912
Ala	Pro	Ala	Arg	Ser	Ala	Ser	Arg	Pro	Arg	Arg	Pro	Val	Glu	Glu	Phe	

290

295

300

<210> 40

<211> 303

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic
construct

<400> 40

Met	Thr	Ser	Arg	Arg	Ser	Val	Lys	Ser	Gly	Pro	Arg	Glu	Val	Pro	Arg
1				5					10					15	

Asp	Glu	Tyr	Glu	Asp	Leu	Tyr	Tyr	Thr	Pro	Ser	Ser	Gly	Met	Ala	Ser
			20					25					30		

Pro	Asp	Ser	Pro	Pro	Asp	Thr	Ser	Arg	Arg	Gly	Ala	Leu	Gln	Thr	Arg
		35					40					45			

Ser	Arg	Gln	Arg	Gly	Glu	Val	Arg	Phe	Val	Gln	Tyr	Asp	Glu	Ser	Asp
	50					55					60				

Tyr	Ala	Leu	Tyr	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	Glu	His	Pro	Glu
65					70					75					80

Val	Pro	Arg	Thr	Arg	Arg	Pro	Val	Ser	Gly	Ala	Val	Leu	Ser	Gly	Pro
				85					90					95	

Gly	Pro	Ala	Arg	Ala	Pro	Pro	Pro	Pro	Ala	Gly	Ser	Gly	Gly	Ala	Gly
			100					105					110		

Arg	Thr	Pro	Thr	Thr	Ala	Pro	Arg	Ala	Pro	Arg	Thr	Gln	Arg	Val	Ala
		115					120					125			

Thr	Lys	Ala	Pro	Ala	Ala	Pro	Ala	Ala	Glu	Thr	Thr	Arg	Gly	Arg	Lys
	130					135					140				

Ser	Ala	Gln	Pro	Glu	Ser	Ala	Ala	Leu	Pro	Asp	Ala	Pro	Ala	Ser	Thr
145					150					155					160

Ala	Pro	Thr	Arg	Ser	Lys	Thr	Pro	Ala	Gln	Gly	Leu	Ala	Arg	Lys	Leu
				165					170					175	

His	Phe	Ser	Thr	Ala	Pro	Pro	Asn	Pro	Asp	Ala	Pro	Trp	Thr	Pro	Arg
			180					185					190		

Val	Ala	Gly	Phe	Asn	Lys	Arg	Val	Phe	Cys	Ala	Ala	Val	Gly	Arg	Leu
		195					200					205			

Ala	Ala	Met	His	Ala	Arg	Met	Ala	Ala	Val	Gln	Leu	Trp	Asp	Met	Ser
		210				215						220			

Arg	Pro	Arg	Thr	Asp	Glu	Asp	Leu	Asn	Glu	Leu	Leu	Gly	Ile	Thr	Thr
225					230					235					240

Ile	Arg	Val	Thr	Val	Cys	Glu	Gly	Lys	Asn	Leu	Leu	Gln	Arg	Ala	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	245		250		255
Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala					
	260		265		270
Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala					
	275		280		285
Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe					
	290		295		300

<210> 41
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4) .. (120)

<400> 41
 cat atg gac gtc gac gcg gcc acg gcg act cga ggg cgt tct gcg gcg 48
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala
 1 5 10 15
 tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc 96
 Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg
 20 25 30
 ccc aga cgg ccc gtc gag gaa ttc 120
 Pro Arg Arg Pro Val Glu Glu Phe
 35

<210> 42
 <211> 39
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 42
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
 1 5 10 15
 Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
 20 25 30
 Arg Arg Pro Val Glu Glu Phe
 35

<210> 43
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
aggaggtgga tctgc

15

<210> 44
<211> 6
<212> PRT
<213> Mus musculus

<400> 44
Glu Arg Met Arg Arg Pro
1 5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<400> 45
Glu Arg Met Pro Pro Arg Arg Asp
1 5

BI
Conclude